

=> fil reg; d que l2

FILE 'REGISTRY' ENTERED AT 10:10:33 ON 02 JUL 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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STRUCTURE FILE UPDATES: 30 JUN 2002 HIGHEST RN 435268-39-6
DICTIONARY FILE UPDATES: 30 JUN 2002 HIGHEST RN 435268-39-6

TSCA INFORMATION NOW CURRENT THROUGH January 7, 2002

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

L2 0 SEA FILE=REGISTRY ABB=ON GCCUGUGCCCGCUGCCGCUGGGCUGUGGCAU|AUGCC
 ACAGCCCAGCGGCAGCGGGCACAGGC/SQSN

=> fil hom

FILE 'HOME' ENTERED AT 10:10:37 ON 02 JUL 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2002, 01:07:06 ; Search time 4716.38 Seconds
(without alignments)
17384.132 Million cell updates/sec

Title: US-09-781-311-1
Perfect score: 3918
Sequence: 1 aaacagagtgtggtcagggg.....cctttgggaacttgggccag 3918

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result		Query							
No.	Score	Match	Length	DB	ID	Description			
c	1	3904.8	99.7	227245	9	AC008569	AC008569 Homo sapi		
	2	1310	33.4	5982	6	AX346950	AX346950 Sequence		
	3	1027.4	26.2	1974	4	AF266477	AF266477 Canis fam		
	4	967	24.7	1376	9	HUMG	L22647 Human prost		
	5	967	24.7	1394	6	AR086516	AR086516 Sequence		
	6	944.4	24.1	1209	6	AX280933	AX280933 Sequence		
c	7	917.4	23.4	5982	6	AX346951	AX346951 Sequence		
c	8	796.2	20.3	123682	2	AC079479	AC079479 Mus muscu		
c	9	788.8	20.1	7233	10	MMPKNEP1	Y07611 M.musculus		
	10	788.2	20.1	221787	2	AC073690	AC073690 Mus muscu		
	11	783.8	20.0	197013	2	AC079552	AC079552 Mus muscu		
c	12	777.8	19.9	179262	2	AC079507	AC079507 Mus muscu		
	13	773.4	19.7	2275	10	MMEP1PRG1	Z49987 M.musculus		
	14	766.8	19.6	2805	10	D88752	D88752 Rattus norv		
	15	642.2	16.4	2216	10	D88751	D88751 Rattus norv		
	16	628	16.0	1312	10	MUSPGEP1S	D16338 Mouse mRNA		
	17	614.4	15.7	1218	10	RNU68037	U68037 Rattus norv		
	18	411.8	10.5	139726	2	AC096306	AC096306 Rattus no		
	19	275.2	7.0	781	4	AF043491	AF043491 Oryctolag		
	20	233.6	6.0	123682	2	AC079479	AC079479 Mus muscu		
	21	182.4	4.7	314	4	AF035415	AF035415 Ovis arie		
	22	154	3.9	1323	9	HSU27325	U27325 Human throm		
	23	152.4	3.9	885	9	HUMTA2R3	D15055 Homo sapien		
	24	152.4	3.9	1492	9	HSU11271	U11271 Human alter		
	25	152.4	3.9	2932	6	E03829	E03829 cDNA encodi		
	26	152.4	3.9	2932	9	HUMHTAR	D38081 Human mRNA		
c	27	152.4	3.9	41303	9	AC005175	AC005175 Homo sapi		
	28	152.4	3.9	175625	2	AC068475	AC068475 Homo sapi		
	29	141.6	3.6	1277	9	AF017452	AF017452 Cercopith		
	30	139.6	3.6	945	4	BTU53485	U53485 Bos taurus		
	31	134.8	3.4	3103	4	AF177934	AF177934 Canis fam		
	32	129.8	3.3	1418	10	RATTA2R	D21158 Rattus norv		
	33	129.8	3.3	1880	10	RATTHA2R	D32080 Rattus norv		
c	34	123.2	3.1	220469	2	AC074307	AC074307 Mus muscu		
	35	122	3.1	1087	10	MMU9969	AJ009969 Mus muscu		
	36	122	3.1	1671	10	MUSTXA2R	D10849 Mus musculu		
c	37	121.4	3.1	303091	2	AC084799	AC084799 Mus muscu		
	38	118.6	3.0	1428	4	BTZ93039	Z93039 B.taurus pr		
c	39	117.4	3.0	298166	2	AC087563	AC087563 Homo sapi		
	40	117.2	3.0	1211	10	RNEP3B	X80133 R.norvegicu		
	41	117.2	3.0	1345	10	RNEP3ALPH	X83855 R.norvegicu		
	42	115.8	3.0	1253	10	RATPEP3R	D29969 Rat mRNA fo		

	43	115.2	2.9	239130	2	AC079420
c	44	112.8	2.9	165556	2	AC087190
	45	111.8	2.9	1860	10	MMEP1PRG2

AC079420	Mus muscu
AC087190	Homo sapi
Z49986	M.musculus

Title: US-09-781-311-1
 Perfect score: 3918
 Sequence: 1 aaacagagtgtgggtcagggg.....cctttgggaacttgggccag 3918

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_032802:*
 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1310	33.4	5982	24	ABL34048	Human immune syste
	2	967	24.7	1376	21	AAF21042	Human low adenosin
	3	967	24.7	1376	21	AAA34920	Human adenosine re

	4	967	24.7	1394	16	AAQ80287	Prostaglandin rece
	5	967	24.7	9060	21	AAF21047	Human low adenosin
	6	967	24.7	9060	21	AAA34925	Human adenosine re
	7	949.2	24.2	1226	21	AAZ93894	Human EP-1 prostag
	8	944.4	24.1	1209	23	ABI98018	Non-endogenous hum
c	9	917.4	23.4	5982	24	ABL34049	Human immune syste
c	10	152.4	3.9	2169	22	AAI58060	Human polynucleoti
	11	152.4	3.9	2932	13	AAQ25388	TXA2 receptor gene
	12	152.4	3.9	2932	20	AAZ32161	Human thromboxane
	13	152.4	3.9	2932	20	AAZ32162	Human endothelial
	14	152.4	3.9	2932	23	AAS65879	DNA encoding novel
c	15	152.4	3.9	9333	22	AAK74093	Human immune/haema
	16	110.8	2.8	1216	21	AAF21227	Human low adenosin
	17	110.8	2.8	1216	21	AAA35105	Human adenosine re
	18	110.8	2.8	1253	22	ABA09244	Human prostaglandi
	19	110.8	2.8	1253	22	AAK53126	Human polynucleoti
	20	110.8	2.8	1264	21	AAA27056	Human cell surface
	21	110.8	2.8	1303	22	AAK52142	Human polynucleoti
	22	110.8	2.8	1488	17	AAT37402	Prostaglandin DP r
	23	110.8	2.8	14607	21	AAF21235	Human low adenosin
	24	110.8	2.8	14607	21	AAA35113	Human adenosine re
	25	110.2	2.8	114955	20	AAX53491	Human adenosine A1
	26	109.8	2.8	1405	14	AAQ46125	PGE2 receptor (EP3
	27	109.8	2.8	2107	14	AAQ46124	PGE2 receptor (EP3
	28	108.4	2.8	1417	16	AAQ91963	Prostaglandin IP r
	29	106.8	2.7	1320	16	AAQ98300	Human prostaglandi
	30	106.8	2.7	1417	21	AAF21234	Human low adenosin
	31	106.8	2.7	1417	21	AAA35112	Human adenosine re
	32	106.8	2.7	1498	16	AAQ91966	hLXR3-11 cDNA. Ho
	33	105.4	2.7	1077	23	ABI98019	Non-endogenous hum
	34	105.4	2.7	2372	21	AAF21041	Human low adenosin
	35	105.4	2.7	2372	21	AAF21228	Human low adenosin
	36	105.4	2.7	2372	21	AAA34919	Human adenosine re
	37	105.4	2.7	2372	21	AAA35106	Human adenosine re
	38	105.4	2.7	6446	20	AAZ24737	Human prostaglandi
	39	105.2	2.7	1979	16	AAQ98298	Human prostaglandi
	40	104.8	2.7	1158	16	AAQ98297	Human prostaglandi
c	41	104	2.7	114955	20	AAX53491	Human adenosine A1
	42	103.8	2.6	1077	21	AAF21043	Human low adenosin
	43	103.8	2.6	1077	21	AAA34921	Human adenosine re
	44	103.8	2.6	2296	19	AAV12457	Human HP4 prostagl
	45	103.2	2.6	1158	16	AAQ98299	Human prostaglandi

Title: US-09-781-311-1
 Perfect score: 3918
 Sequence: 1 aaacagagtgtgggtcagggg.....cctttgggaacttgggccag 3918

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				Description
	No.	Score	Match	Length	DB	ID	
	1	967	24.7	1394	2	US-08-068-729-3	Sequence 3, Appli
	2	967	24.7	1394	3	US-09-255-671-3	Sequence 3, Appli
	3	110.8	2.8	1488	2	US-08-812-203-4	Sequence 4, Appli
	4	110.8	2.8	1488	4	US-09-300-864-4	Sequence 4, Appli
	5	110.6	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	6	109.8	2.8	1405	1	US-08-390-162-3	Sequence 3, Appli
	7	109.8	2.8	1405	1	US-08-685-945B-3	Sequence 3, Appli
	8	109.8	2.8	2107	1	US-08-390-162-1	Sequence 1, Appli
	9	109.8	2.8	2107	1	US-08-685-945B-1	Sequence 1, Appli
	10	106.8	2.7	1417	1	US-08-134-012-4	Sequence 4, Appli
	11	106.8	2.7	1417	1	US-08-520-519-4	Sequence 4, Appli
	12	106.8	2.7	1498	1	US-08-134-012-6	Sequence 6, Appli
	13	106.8	2.7	1498	1	US-08-520-519-6	Sequence 6, Appli
	14	103.8	2.6	2296	1	US-08-239-431A-3	Sequence 3, Appli
	15	103.2	2.6	1356	1	US-08-134-012-5	Sequence 5, Appli
	16	103.2	2.6	1356	1	US-08-520-519-5	Sequence 5, Appli
c	17	99.8	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	18	97.8	2.5	1074	2	US-08-463-081B-29	Sequence 29, Appl
	19	97.8	2.5	1074	2	US-08-461-379A-29	Sequence 29, Appl
	20	97.8	2.5	1074	2	US-08-462-390B-29	Sequence 29, Appl
	21	97.8	2.5	1074	3	US-08-463-074B-29	Sequence 29, Appl
	22	97.8	2.5	1074	3	US-08-465-585C-29	Sequence 29, Appl

	23	97.8	2.5	1074	3	US-08-652-446-29	Sequence 29, Appl
	24	97.8	2.5	1119	1	US-08-416-756A-1	Sequence 1, Appli
	25	97.8	2.5	1223	3	US-08-155-005A-5	Sequence 5, Appli
	26	97.8	2.5	1223	4	US-09-363-783-5	Sequence 5, Appli
	27	97.8	2.5	1429	3	US-08-155-005A-7	Sequence 7, Appli
	28	97.8	2.5	1429	4	US-09-363-783-7	Sequence 7, Appli
	29	97.8	2.5	1651	3	US-08-155-005A-3	Sequence 3, Appli
	30	97.8	2.5	1651	4	US-09-363-783-3	Sequence 3, Appli
	31	97.8	2.5	1729	3	US-08-155-005A-16	Sequence 16, Appl
	32	97.8	2.5	1729	4	US-09-363-783-16	Sequence 16, Appl
	33	97.8	2.5	2450	2	US-08-463-081B-5	Sequence 5, Appli
	34	97.8	2.5	2450	2	US-08-461-379A-5	Sequence 5, Appli
	35	97.8	2.5	2450	2	US-08-462-390B-5	Sequence 5, Appli
	36	97.8	2.5	2450	3	US-08-463-074B-5	Sequence 5, Appli
	37	97.8	2.5	2450	3	US-08-465-585C-5	Sequence 5, Appli
	38	97.8	2.5	2450	3	US-08-652-446-5	Sequence 5, Appli
	39	96.4	2.5	2906	1	US-08-554-612C-49	Sequence 49, Appl
	40	85.2	2.2	1958	1	US-08-115-365-1	Sequence 1, Appli
	41	85.2	2.2	1958	1	US-08-586-897-1	Sequence 1, Appli
	42	81.2	2.1	4897	6	5196516-7	Patent No. 5196516
c	43	80.4	2.1	2580	3	US-09-050-863-2	Sequence 2, Appli
c	44	80.4	2.1	2580	4	US-09-359-081-2	Sequence 2, Appli
	45	80.4	2.1	5452	2	US-09-130-114-1	Sequence 1, Appli

Title: US-09-781-311-1
 Perfect score: 3918
 Sequence: 1 aaacagagtgtgggtcagggg.....cctttgggaacttgggccag 3918

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: em_estba:*
 2: em_esthum:*
 3: em_estin:*
 4: em_estmu:*
 5: em_estov:*
 6: em_estpl:*
 7: em_estro:*
 8: em_htc:*
 9: gb_est1:*
 10: gb_est2:*
 11: gb_htc:*
 12: gb_gss:*
 13: em_gss_hum:*
 14: em_gss_inv:*
 15: em_gss_pln:*
 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	561.8	14.3	671	10	BE256373	BE256373 601117831	
2	530.8	13.5	661	9	AW058596	AW058596 wx23h03.x	
3	518.8	13.2	775	9	AI480353	AI480353 tm51d04.x	
4	514.2	13.1	677	9	AW026977	AW026977 wv64d07.x	
5	510.2	13.0	577	9	AW304137	AW304137 xs13g01.x	
6	505.2	12.9	605	9	AI936469	AI936469 wd28c10.x	
7	500.6	12.8	632	9	AW300310	AW300310 xs59f03.x	
8	494.8	12.6	532	9	AI627838	AI627838 ty82f08.x	
9	492.4	12.6	543	10	BF115139	BF115139 hr74h06.x	
10	489.2	12.5	712	9	AI634807	AI634807 wa08a11.x	
11	488.8	12.5	765	9	AI796157	AI796157 wh43c03.x	

	12	475.8	12.1	511	10	BE501427	BE501427 hw31f01.x
c	13	444.8	11.4	499	9	AI521865	AI521865 ti83d06.x
c	14	440.6	11.2	554	10	BF511364	BF511364 UI-H-BI4-
c	15	440.2	11.2	453	9	AI470837	AI470837 ti89f10.x
c	16	433.8	11.1	478	9	AI935642	AI935642 wo99a01.x
	17	432.4	11.0	508	10	BI760106	BI760106 603044593
c	18	429	10.9	429	10	BM127301	BM127301 ie97d03.x
c	19	428.4	10.9	442	10	BF197413	BF197413 hr80b11.x
c	20	422.2	10.8	491	9	AI765899	AI765899 wh66h07.x
c	21	419.4	10.7	472	9	AI762344	AI762344 wg97c05.x
c	22	414.8	10.6	430	10	BM069600	BM069600 ie90c03.x
	23	412.2	10.5	436	10	BM069845	BM069845 ie90c03.y
	24	411.4	10.5	415	10	BF515800	BF515800 UI-H-BW1-
c	25	407.8	10.4	443	9	AW269162	AW269162 xs33b01.x
	26	407.4	10.4	428	10	BM127603	BM127603 ie97d03.y
	27	400.8	10.2	645	12	AZ710496	AZ710496 RPCI-24-1
	28	396.2	10.1	683	9	BB665255	BB665255 BB665255
c	29	388.8	9.9	409	10	BF447978	BF447978 hr83f03.x
c	30	388.2	9.9	451	9	AI953667	AI953667 wq23h11.x
c	31	387	9.9	444	9	AW237821	AW237821 xm83a02.x
c	32	385.4	9.8	441	9	AI572850	AI572850 tn50h06.x
c	33	380.4	9.7	781	10	BI413305	BI413305 602986485
c	34	374.8	9.6	418	10	BM127241	BM127241 ie96e02.x
c	35	365.2	9.3	766	10	BG261811	BG261811 602373607
c	36	364.6	9.3	445	9	AI590344	AI590344 tn49c12.x
	37	363	9.3	731	9	BB603028	BB603028 BB603028
c	38	362	9.2	362	9	AI522201	AI522201 ti84d06.x
c	39	340.8	8.7	395	9	AI953039	AI953039 wq49e07.x
	40	340.6	8.7	392	10	BM055340	BM055340 ie93e12.y
c	41	339.4	8.7	341	9	AW614116	AW614116 hg75g06.x
c	42	335	8.6	335	9	AW015286	AW015286 UI-H-BI0-
	43	319.8	8.2	514	10	BM054533	BM054533 id52c10.y
c	44	317.2	8.1	447	10	BE689265	BE689265 uw51f04.y
c	45	311.6	8.0	360	9	AI203170	AI203170 qr34f05.x